```
┌─────────────────────────────────────────────────────────────────┐
│     SCORE Search Results Details for Application                  │
│     10679362 and Search Result us-10-679-362-                     │
│                        1.rng.                                     │
└─────────────────────────────────────────────────────────────────┘
```

| Score Home Page | Retrieve Application List | SCORE System Overview | SCORE FAQ | Comments / Suggestions |

This page gives you Search Results detail for the Application 10679362 and Search Result us-10-679-362-1.rng.

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```
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OM nucleic - nucleic search, using sw model

Run on:        August  7, 2006, 13:36:04 ; Search time 1314 Seconds
                                        (without alignments)
                                        11105.720 Million cell updates/sec

Title:         US-10-679-362-1
Perfect score: 2093
Sequence:      1 cgggcagcaaaggaggatgg..........aaaaaaaaaaaaaaaaaaaa 2093

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters:       10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     N_Geneseq_8:*
               1:  geneseqn1980s:*
               2:  geneseqn1990s:*
               3:  geneseqn2000s:*
               4:  geneseqn2001as:*
               5:  geneseqn2001bs:*
               6:  geneseqn2002as:*
               7:  geneseqn2002bs:*
               8:  geneseqn2003as:*
               9:  geneseqn2003bs:*
               10:  geneseqn2003cs:*
               11:  geneseqn2003ds:*
               12:  geneseqn2004as:*
               13:  geneseqn2004bs:*
               14:  geneseqn2005s:*
               15:  geneseqn2006s:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                           SUMMARIES
```

| | | % Query | | | | |
Result No.	Score	Match	Length	DB	ID	Description
1	2093	100.0	2093	10	ADF90163	Adf90163 cDNA enco
2	2093	100.0	2093	13	ADR03798	Adr03798 Human cDN
3	1847.6	88.3	2057	8	ABZ80236	Abz80236 Human tra
4	1806.4	86.3	5821	14	ADZ49865	Adz49865 Insulin s
5	1806	86.3	2807	8	ABX12019	Abx12019 Transport
6	1609.8	76.9	3114	6	AAL44674	Aal44674 Human tra
7	1541.8	73.7	1961	10	ADA53869	Ada53869 Human cod
8	1541.8	73.7	1961	13	ADS10331	Ads10331 Human the
9	1498.4	71.6	1597	8	ABX70783	Abx70783 Novel hum
10	1441.8	68.9	1501	10	ABX70643	Abx70643 Human cDN
11	1363.8	65.2	1513	10	ABX70642	Abx70642 Human cDN
12	1327.2	63.4	1428	4	ABL57930	Abl57930 Human VG5
13	1133	54.1	1784	4	ABL57913	Abl57913 Rat VG51

```
┌─────────────────────────────────────────────────────────────┐
│   SCORE Search Results Details for Application                │
│   10679362 and Search Result us-10-679-362-                   │
│                      1.rge.                                    │
└─────────────────────────────────────────────────────────────┘
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| Score Home Page | Retrieve Application List | SCORE System Overview | SCORE FAQ | Comments / Suggestions |

This page gives you Search Results detail for the Application 10679362 and Search Result us-10-679-362-1.rge.

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OM nucleic - nucleic search, using sw model

Run on:        August  7, 2006, 13:37:36 ; Search time 19131 Seconds
                                          (without alignments)
                               6996.077 Million cell updates/sec

Title:         US-10-679-362-1
Perfect score: 2093
Sequence:      1 cgggcagcaaaggaggatgg.........aaaaaaaaaaaaaaaaaaaa 2093

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters:      12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     GenEmbl:*
               1:  gb_env:*
               2:  gb_pat:*
               3:  gb_ph:*
               4:  gb_pl:*
               5:  gb_pr:*
               6:  gb_ro:*
               7:  gb_sts:*
               8:  gb_sy:*
               9:  gb_un:*
               10: gb_vi:*
               11: gb_ov:*
               12: gb_htg:*
               13: gb_in:*
               14: gb_om:*
               15: gb_ba:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
```

| | | % Query | | | | | |
Result No.	Score	Match	Length	DB	ID	Description
1	1806	86.3	5823	5	HSM806092	BX537963 Homo sapi
2	1791.6	85.6	5585	5	AF516142	AF516142 Homo sapi
3	1691.2	80.8	2028	5	AB168788	AB168788 Macaca fa
4	1609.8	76.9	3114	2	AX686980	AX686980 Sequence
5	1585.4	75.7	1710	5	AY162213	AY162213 Homo sapi
6	1541.8	73.7	1961	2	AX714753	AX714753 Sequence
7	1541.8	73.7	1961	5	AK057340	AK057340 Homo sapi
8	1498.4	71.6	1597	2	AR541761	AR541761 Sequence
9	1498.4	71.6	1597	2	AR698923	AR698923 Sequence
10	1441.8	68.9	1501	2	AX717763	AX717763 Sequence
11	1370	65.5	2296	14	AY989816	AY989816 Oryctolag
12	1363.8	65.2	1513	2	AX717761	AX717761 Sequence
13	1327.2	63.4	1428	2	AX049362	AX049362 Sequence

SCORE Search Results Details for Application 10679362 and Search Result us-10-679-362-1.rst.

This page gives you Search Results detail for the Application 10679362 and Search Result us-10-679-362-1.rst.

start

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OM nucleic - nucleic search, using sw model

Run on:        August  7, 2006, 13:56:43 ; Search time 9987 Seconds
                                          (without alignments)
                                          11719.151 Million cell updates/sec

Title:         US-10-679-362-1
Perfect score: 2093
Sequence:      1 cgggcagcaaaggaggatgg..........aaaaaaaaaaaaaaaaaaaa 2093

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:      48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters:      96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     EST:*
               1:  gb_est1:*
               2:  gb_est3:*
               3:  gb_est4:*
               4:  gb_est5:*
               5:  gb_est6:*
               6:  gb_htc:*
               7:  gb_est2:*
               8:  gb_est7:*
               9:  gb_est8:*
               10:  gb_est9:*
               11:  gb_gss1:*
               12:  gb_gss2:*
               13:  gb_gss3:*
               14:  gb_gss4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                    %
Result          Query
No.      Score  Match Length DB   ID                      Description
-----------------------------------------------------------------------------
     1    1266   60.5   1482  14   DQ050191            DQ050191 Homo sapi
     2  1235.6   59.0   1481  14   DQ050192            DQ050192 Pan trogl
     3   867.6   41.5   3404   6   CR859927            CR859927 Pongo pyg
     4   833.6   39.8   2412   6   AK156409            AK156409 Mus muscu
     5   833.6   39.8   2422   6   AK041041            AK041041 Mus muscu
     6    832    39.8   1632   6   AK160394            AK160394 Mus muscu
     7    832    39.8   2371   6   AK079053            AK079053 Mus muscu
     8   707.2   33.8    790   1   AL043182            AL043182 DKFZp434G
     9   638.4   30.5   2481  14   DQ039367            DQ039367 Homo sapi
    10   623.6   29.8   1844   6   AK132910            AK132910 Mus muscu
    11   614.4   29.4    632   3   BM696484            BM696484 UI-E-DWO-
    12   605.6   28.9   2475  14   DQ039368            DQ039368 Pan trogl
    13   601.6   28.7   1280   5   CJ105223            CJ105223 CJ105223
    14   582.8   27.8    747   5   CK634094            CK634094 UI-M-HNO-
```

SCORE Search Results Details for Application 10679362 and Search Result us-10-679-362-1.rni.

Score Home Page	Retrieve Application List	SCORE System Overview	SCORE FAQ	Comments / Suggestions

This page gives you Search Results detail for the Application 10679362 and Search Result us-10-679-362-1.rni.

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```
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OM nucleic - nucleic search, using sw model

Run on:        August  7, 2006, 13:58:37 ; Search time 416 Seconds
                                  (without alignments)
                                  9414.016 Million cell updates/sec

Title:         US-10-679-362-1
Perfect score: 2093
Sequence:      1 cgggcagcaaaggaggatgg..........aaaaaaaaaaaaaaaaaaaa 2093

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters:      2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     Issued_Patents_NA:*
               1:  /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
               2:  /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
               3:  /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
               4:  /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
               5:  /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
               6:  /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
               7:  /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
               8:  /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
               9:  /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
               10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result         Query
  No.   Score  Match Length DB  ID                   Description
-------------------------------------------------------------------------
    1  1541.8  73.7   1961  4   US-10-094-749-1437   Sequence 1437, Ap
    2  1498.4  71.6   1597  3   US-09-774-528-9      Sequence 9, Appli
    3  1498.4  71.6   1597  3   US-10-120-988-9      Sequence 9, Appli
    4   467.4  22.3   2363  3   US-09-178-093B-25    Sequence 25, Appl
    5   379.6  18.1   1455  4   US-10-154-419-93     Sequence 93, Appl
    6   379.6  18.1   2397  4   US-10-154-419-91     Sequence 91, Appl
    7   165.6   7.9    176  3   US-09-621-976-13903  Sequence 13903, A
    8   120.6   5.8   1696  3   US-09-835-811-1      Sequence 1, Appli
    9   120     5.7   3275  3   US-09-370-838-151    Sequence 151, App
   10   120     5.7   3275  3   US-09-854-133-151    Sequence 151, App
   11   119.4   5.7    882  3   US-09-311-021-107    Sequence 107, App
   12   119.2   5.7   1459  3   US-09-537-654-3      Sequence 3, Appli
   13   119.2   5.7   1459  5   US-10-818-809-3      Sequence 3, Appli
   14   118.6   5.7    674  3   US-09-620-405B-465   Sequence 465, App
   15   118.6   5.7    674  3   US-09-433-826B-465   Sequence 465, App
   16   118.6   5.7    674  3   US-09-604-287A-465   Sequence 465, App
   17   118.6   5.7    674  3   US-09-834-759-465    Sequence 465, App
   18   118.6   5.7    674  3   US-09-590-751A-465   Sequence 465, App
```

SCORE Search Results Details for Application 10679362 and Search Result us-10-679-362-2.p2n.rng.

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This page gives you Search Results detail for the Application 10679362 and Search Result us-10-679-362-2.p2n.rng.

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                          GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on:        August  7, 2006, 14:03:26 ; Search time 1150 Seconds
                                           (without alignments)
                                           4328.857 Million cell updates/sec

Title:         US-10-679-362-2
Perfect score: 2469
Sequence:      1 MSTQRLRNEDYHDYSSTDVS..........YELIQPSNAPIFINSTCAFI 476

Scoring table: BLOSUM62
               Xgapop 10.0 , Xgapext  0.5
               Ygapop 10.0 , Ygapext  0.5
               Fgapop  6.0 , Fgapext  7.0
               Delop   6.0 , Delext   7.0

Searched:      5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters:      10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10679362/runat_07082006_113044_25898/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss06p
-USER=US10679362_@CGN_1_1_1147_@runat_07082006_113044_25898 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :     N_Geneseq_8:*
               1:  geneseqn1980s:*
               2:  geneseqn1990s:*
               3:  geneseqn2000s:*
               4:  geneseqn2001as:*
               5:  geneseqn2001bs:*
               6:  geneseqn2002as:*
               7:  geneseqn2002bs:*
               8:  geneseqn2003as:*
               9:  geneseqn2003bs:*
               10:  geneseqn2003cs:*
               11:  geneseqn2003ds:*
               12:  geneseqn2004as:*
               13:  geneseqn2004bs:*
               14:  geneseqn2005s:*
               15:  geneseqn2006s:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                          SUMMARIES

Result           Query
```

No.	Score	Match	Length	DB	ID	Description
1	2469	100.0	1597	8	ABX70783	Abx70783 Novel hum
2	2469	100.0	2057	8	ABZ80236	Abz80236 Human tra
3	2469	100.0	2093	10	ADF90163	Adf90163 cDNA enco
4	2469	100.0	2093	13	ADR03798	Adr03798 Human cDN
5	2469	100.0	5821	14	ADZ49865	Adz49865 Insulin s
6	2466	99.9	2807	8	ABX12019	Abx12019 Transport
7	2460	99.6	1501	10	ABX70643	Abx70643 Human cDN
8	2402.5	97.3	3114	6	AAL44674	Aal44674 Human tra
9	2398	97.1	1513	10	ABX70642	Abx70642 Human cDN
10	2324	94.1	1428	4	ABL57930	Abl57930 Human VG5
11	2217	89.8	1961	10	ADA53869	Ada53869 Human cod
12	2217	89.8	1961	13	ADS10331	Ads10331 Human the
13	2146.5	86.9	1824	8	ABZ80241	Abz80241 Rat LYAAT
14	2144.5	86.9	1625	8	ABZ80238	Abz80238 Mouse tra
15	2142.5	86.8	1784	4	ABL57913	Abl57913 Rat VG51
16	1959	79.3	1889	4	ABL57912	Abl57912 Rat VG41
17	1722.5	69.8	1619	6	ABQ79491	Abq79491 Human HIP
18	1722.5	69.8	3434	8	ABZ80230	Abz80230 Human tra
19	1718.5	69.6	1464	6	AAD44327	Aad44327 Human tra
20	1718.5	69.6	1593	13	ADN33180	Adn33180 Human tra
21	1718.5	69.6	2142	8	AAD47354	Aad47354 Human tra
22	1713.5	69.4	2444	12	ADQ63759	Adq63759 Novel hum
23	1678.5	68.0	2421	8	ABZ80228	Abz80228 Rat tramd
24	1551.5	62.8	2108	12	ADJ27245	Adj27245 Human TRI
25	1544	62.5	1520	6	ABQ79492	Abq79492 Human HIP
26	1539	62.3	2083	12	ADJ27264	Adj27264 Human TRI
27	1476.5	59.8	1703	8	ABZ80231	Abz80231 Human tra
28	1476.5	59.8	2456	13	ADR07759	Adr07759 Full leng
29	1463	59.3	1299	12	ADP28269	Adp28269 Human sec
30	1461	59.2	1293	12	ADP28425	Adp28425 Human sec
31	1452.5	58.8	1473	6	AAD41820	Aad41820 Human tra
32	1420	57.5	1752	8	ABZ80237	Abz80237 Mouse tra
33	1375.5	55.7	1557	13	ADS10330	Ads10330 Human the
34	1333.5	54.0	947	5	ABV23244	Abv23244 Human pro
35	1333.5	54.0	947	5	ABV29088	Abv29088 Human pro
36	1301	52.7	3558	12	ADQ67469	Adq67469 Novel hum
37	1293.5	52.4	3573	4	ABL57910	Abl57910 Rat VG1 c
38	1263	51.2	953	10	ABX70644	Abx70644 Human cDN
39	1263	51.2	1098	13	ADS11640	Ads11640 Human the
40	1263	51.2	1098	13	ADS11639	Ads11639 Human the
41	1255.5	50.9	1455	10	ADD37512	Add37512 Human tra
42	1255.5	50.9	2366	4	AAI59840	Aai59840 Human pol
43	1255.5	50.9	2397	8	ABV72444	Abv72444 Nucleotid
44	1255.5	50.9	2397	10	ADD37510	Add37510 Human tra
45	1255.5	50.9	2423	4	AAI58054	Aai58054 Human pol

ALIGNMENTS

RESULT 1
ABX70783
ID   ABX70783 standard; cDNA; 1597 BP.
XX
AC   ABX70783;
XX
DT   05-MAR-2003   (first entry)
XX
DE   Novel human cDNA sequence #8.
XX
KW   Human; gene; ss; nervous system disorder; peripheral neuropathy;
KW   Huntington's disease; amyotrophic lateral sclerosis; haemophilia;
KW   neurodegenerative disease; Parkinson's disease; Alzheimer's disease;
KW   autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis;
KW   insulin-dependent diabetes mellitus; anaemia; thrombocytopaenia; wound;
KW   ulcer; burn; bone disorder; osteoporosis; osteoarthritis; stroke;
KW   fibrosis; reperfusion injury; infection; allergic rhinitis; asthma;
KW   coagulation disorder; cancer; tumour; inflammatory disease; septic shock;
KW   Crohn's disease; anaphylaxis; proliferation; chemotactic;
KW   differentiation; stem cell growth factor; haematopoiesis; chemokinetic;
KW   haemostatic; antiinflammatory; expressed sequence tag; EST.
XX
OS   Homo sapiens.
XX
PN   WO200281731-A2.
XX
PD   17-OCT-2002.
XX
PF   29-JAN-2002; 2002WO-US001222.
XX
PR   30-JAN-2001; 2001US-00774528.
XX
PA   (HYSE-) HYSEQ INC.
PA   (GOOD/) GOODRICH R W.
XX
PI   Tang TY, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI   Xue AJ, Yang Y, Wehrman T, Wang J, Wang D, Drmanac RT;
XX
DR   WPI; 2003-058563/05.
XX

SCORE Search Results Details for Application 10679362 and Search Result us-10-679-362-2.p2n.rst.

Score Home Page | Retrieve Application List | SCORE System Overview | SCORE FAQ | Comments / Suggestions

This page gives you Search Results detail for the Application 10679362 and Search Result us-10-679-362-2.p2n.rst.

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```
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OM protein - nucleic search, using frame_plus_p2n model

Run on:         August  7, 2006, 14:31:09 ; Search time 6639 Seconds
                                          (without alignments)
                                          6013.918 Million cell updates/sec

Title:          US-10-679-362-2
Perfect score:  2469
Sequence:       1 MSTQRLRNEDYHDYSSTDVS..........YELIQPSNAPIFINSTCAFI 476

Scoring table:  BLOSUM62
                Xgapop 10.0 , Xgapext  0.5
                Ygapop 10.0 , Ygapext  0.5
                Fgapop  6.0 , Fgapext  7.0
                Delop   6.0 , Delext   7.0

Searched:       48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters:      96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10679362/runat_07082006_113047_25946/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss04
-USER=US10679362_@CGN_1_1_6323_@runat_07082006_113047_25946 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :      EST:*
                1:  gb_est1:*
                2:  gb_est3:*
                3:  gb_est4:*
                4:  gb_est5:*
                5:  gb_est6:*
                6:  gb_htc:*
                7:  gb_est2:*
                8:  gb_est7:*
                9:  gb_est8:*
                10:  gb_est9:*
                11:  gb_gss1:*
                12:  gb_gss2:*
                13:  gb_gss3:*
                14:  gb_gss4:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                        SUMMARIES
                  %
Result          Query
   No.   Score  Match Length DB  ID                       Description
```

SCORE Search Results Details for Application 10679362 and Search Result us-10-679-362-2.p2n.rge.

This page gives you Search Results detail for the Application 10679362 and Search Result us-10-679-362-2.p2n.rge.

start

```
                        GenCore version 5.1.9
             Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM protein - nucleic search, using frame_plus_p2n model

Run on:        August  7, 2006, 14:09:14 ; Search time 8148 Seconds
                                    (without alignments)
                                    5603.640 Million cell updates/sec

Title:         US-10-679-362-2
Perfect score: 2469
Sequence:      1 MSTQRLRNEDYHDYSSTDVS..........YELIQPSNAPIFINSTCAFI 476

Scoring table: BLOSUM62
               Xgapop 10.0 , Xgapext  0.5
               Ygapop 10.0 , Ygapext  0.5
               Fgapop  6.0 , Fgapext  7.0
               Delop   6.0 , Delext   7.0

Searched:      6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters:      12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10679362/runat_07082006_113045_25911/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss04
-USER=US10679362_@CGN_1_1_5548_@runat_07082006_113045_25911 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :     GenEmbl:*
               1:  gb_env:*
               2:  gb_pat:*
               3:  gb_ph:*
               4:  gb_pl:*
               5:  gb_pr:*
               6:  gb_ro:*
               7:  gb_sts:*
               8:  gb_sy:*
               9:  gb_un:*
               10: gb_vi:*
               11: gb_ov:*
               12: gb_htg:*
               13: gb_in:*
               14: gb_om:*
               15: gb_ba:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                            SUMMARIES
                    %
Result          Query
```

```
No.    Score  Match Length DB   ID                    Description
-----------------------------------------------------------------------------
  1    2469   100.0  1597   2   AR541761              AR541761 Sequence
  2    2469   100.0  1597   2   AR698923              AR698923 Sequence
  3    2469   100.0  1710   5   AY162213              AY162213 Homo sapi
  4    2469   100.0  5823   5   HSM806092             BX537963 Homo sapi
  5    2460    99.6  1501   2   AX717763              AX717763 Sequence
  6    2439    98.8  2028   5   AB168788              AB168788 Macaca fa
  7    2438    98.7  5585   5   AF516142              AF516142 Homo sapi
  8  2402.5    97.3  3114   2   AX686980              AX686980 Sequence
  9    2398    97.1  1513   2   AX717761              AX717761 Sequence
 10    2324    94.1  1428   2   AX049362              AX049362 Sequence
 11  2317.5    93.9  2296  14   AY989816               AY989816 Oryctolag
 12    2217    89.8  1961   2   AX714753              AX714753 Sequence
 13    2217    89.8  1961   5   AK057340              AK057340 Homo sapi
 14  2146.5    86.9  1824   6   AF361239              AF361239 Rattus no
 15  2142.5    86.8  1784   2   AX049344              AX049344 Sequence
 16  2141.5    86.7  1611   6   AF453743              AF453743 Mus muscu
 17  2137.5    86.6  2034   6   AY211262              AY211262 Mus muscu
 18    2029    82.2  1402   5   AY227111              AY227111 Homo sapi
 19    1959    79.3  1889   2   AX049343              AX049343 Sequence
 20  1722.5    69.8  2140   5   BC101103              BC101103 Homo sapi
 21  1722.5    69.8  2142   5   BC101101              BC101101 Homo sapi
 22  1718.5    69.6  1464   2   AX555035              AX555035 Sequence
 23  1718.5    69.6  2142   2   AX575471              AX575471 Sequence
 24  1713.5    69.4  2444   2   CQ842273              CQ842273 Sequence
 25  1713.5    69.4  2444   5   AK122630              AK122630 Homo sapi
 26  1711.5    69.3  3407   5   AY162214              AY162214 Homo sapi
 27  1700.5    68.9  2420   6   BC044800              BC044800 Mus muscu
 28  1697.5    68.8  2357   6   AF453744              AF453744 Mus muscu
 29  1697.5    68.8  2456   6   AF512429              AF512429 Mus muscu
 30  1689.5    68.4  2767  11   BC070857               BC070857 Xenopus 1
 31  1678.5    68.0  2436   6   AF512430              AF512430 Rattus no
 32    1623    65.7   925   2   CQ728082              CQ728082 Sequence
 33    1592    64.5  1420   5   AY227112              AY227112 Homo sapi
 34  1556.5    63.0  2057   5   BC101102              BC101102 Homo sapi
 35  1515.5    61.4  2156   5   BC101100              BC101100 Homo sapi
 36  1476.5    59.8  1597   5   BC101095              BC101095 Homo sapi
 37  1476.5    59.8  2268   5   AY162215              AY162215 Homo sapi
 38  1476.5    59.8  2456   2   CQ850796              CQ850796 Sequence
 39  1476.5    59.8  2456   5   AK127978              AK127978 Homo sapi
 40  1472.5    59.6  1597   5   BC101094              BC101094 Homo sapi
 41  1452.5    58.8  1473   2   AX571858              AX571858 Sequence
 42  1450.5    58.7  1751   6   BC097463              BC097463 Rattus no
 43    1447    58.6  1720   5   BC101092              BC101092 Homo sapi
 44    1447    58.6  1720   5   BC101093              BC101093 Homo sapi
 45    1420    57.5  1752   6   AY211261              AY211261 Mus muscu
```

                              ALIGNMENTS

RESULT 1
AR541761
LOCUS   AR541761   1597 bp   DNA   linear   PAT 08-OCT-2004
DEFINITION   Sequence 9 from patent US 6743619.
ACCESSION   AR541761
VERSION   AR541761.1 GI:53933841
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 1597)
  AUTHORS   Tang,Y.T., Zhou,P., Goodrich,R., Liu,C., Asundi,V., Ren,F.,
             Zhang,J., Zhao,Q.A., Yang,Y., Xue,A.J., Wehrman,T., Wang,J.-R.,
             Wang,D. and Drmanac,R.T.
  TITLE   Nucleic acids and polypeptides
  JOURNAL   Patent: US 6743619-A 9 01-JUN-2004;
             Nuvelo; Sunnyvale, CA;
             WOX;
FEATURES   Location/Qualifiers
     source   1. .1597
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:   5.37e-247   Length: 1597
Score: 2469.00   Matches: 476
Percent Similarity: 100.0%   Conservative: 0
Best Local Similarity: 100.0%   Mismatches: 0
Query Match: 100.0%   Indels: 0
DB: 2   Gaps: 0

US-10-679-362-2 (1-476) x AR541761 (1-1597)

Qy   1 MetSerThrGlnArgLeuArgAsnGluAspTyrHisAspTyrSerSerThrAspValSer 20
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Db   103 ATGTCCACGCAGAGACTTCGGAATGAAGACTACCACGACTACAGCTCCACGGACGTGAGC 162

Qy   21 ProGluGluSerProSerGluGlyLeuAsnAsnLeuSerSerProGlySerTyrGlnArg 40
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

SCORE Search Results Details for Application 10679362 and Search Result us-10-679-362-2.p2n.rni.

Score Home Page   Retrieve Application List   SCORE System Overview   SCORE FAQ   Comments / Suggestions

This page gives you Search Results detail for the Application 10679362 and Search Result us-10-679-362-2.p2n.rni.

start

Go Back to previous page

```
                      GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on:        August  7, 2006, 14:45:41 ; Search time 278 Seconds
                                      (without alignments)
                                      4805.654 Million cell updates/sec

Title:         US-10-679-362-2
Perfect score: 2469
Sequence:      1 MSTQRLRNEDYHDYSSTDVS..........YELIQPSNAPIFINSTCAFI 476

Scoring table: BLOSUM62
               Xgapop 10.0 , Xgapext  0.5
               Ygapop 10.0 , Ygapext  0.5
               Fgapop  6.0 , Fgapext  7.0
               Delop   6.0 , Delext   7.0

Searched:      1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters:      2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10679362/runat_07082006_113049_25988/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss03h -USER=US10679362_@CGN_1_1_204_@runat_07082006_113049_25988
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Database :     Issued_Patents_NA:*
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               4:  /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
               5:  /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
               6:  /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
               7:  /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
               8:  /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
               9:  /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
               10:  /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result             Query
  No.    Score  Match Length  DB    ID                    Description
----------------------------------------------------------------------------
     1    2469  100.0   1597   3   US-09-774-528-9        Sequence 9, Appli
     2    2469  100.0   1597   3   US-10-120-988-9        Sequence 9, Appli
     3    2217   89.8   1961   4   US-10-094-749-1437     Sequence 1437, Ap
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